

OIKE

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/758,003

DATE: 07/30/2001

TIME: 12:09:42

Input Set : N:\Crif3\RULE60\09758003.txt

Output Set: N:\CRF3\07302001\I758003.raw

SEQUENCE LISTING

ENTERED

2 (1) GENERAL INFORMATION:

3 (i) APPLICANT: BATCHWAL, VIJAY R

4 HUANG, JIANNING

5 HUI, HAILING

6 GREDDEL, DAVID V

7 (ii) TITLE OF INVENTION: RFP: NOVEL HUMAN PROTEIN INVOLVED IN

8 TUMOR NECROSIS FACTOR SIGNAL TRANSDUCTION, AND SCREENING

9 ASSAYS

10 (iii) NUMBER OF SEQUENCES: 2

11 (iv) CORRESPONDENCE ADDRESS:

12 (A) ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP

13 (B) STREET: 15 GEMISE DRIVE

14 (C) CITY: HILLSBOROUGH

15 (D) STATE: CALIFORNIA

16 (E) COUNTRY: USA

17 (F) ZIP: 94010

18 (v) COMPUTER READABLE FORM:

19 (A) MEDIUM TYPE: Floppy disk

20 (B) COMPUTER: IBM PC compatible

21 (C) OPERATING SYSTEM: PC-DOS,MS-DOS

22 (D) SOFTWARE: PatentIn Release #1.0, Version #1.30

23 (vi) CURRENT APPLICATION DATA:

C--> 24 (A) APPLICATION NUMBER: US/09/758,003

C--> 25 (B) FILING DATE: 09-Jan-2001

26 (C) CLASSIFICATION:

27 (vii) PRIOR APPLICATION DATA:

28 (A) APPLICATION NUMBER: 09/132,113

29 (B) FILING DATE:

30

31 (viii) ATTORNEY/AGENT INFORMATION:

32 (A) NAME: OSMAN, RICHARD A.

33 (B) REGISTRATION NUMBER: 36,627

34 (C) REFERENCE/DOCKET NUMBER: T95-006-1

35 (ix) TELECOMMUNICATION INFORMATION:

36 (A) TELEPHONE: (650) 343-4341

37 (B) TELEFAX: (650) 343-4342

38

41 (2) INFORMATION FOR SEQ ID NO: 1:

42 (i) SEQUENCE CHARACTERISTICS:

43 (A) LENGTH: 2016 base pairs

44 (B) TYPE: nucleic acid

45 (C) STRANDEDNESS: double

46 (D) TOPOLOGY: linear

47 (ii) MOLECULE TYPE: cDNA

48 (ix) FEATURE:

49 (A) NAME/KEY: CDS

50 (B) LOCATION: 1...1013

51 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

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52	ATG	CAA	CCA	GAT	ATG	TCC	TTG	AAT	GTC	ATT	AAG	ATG	AAA	TCC	AAT	GAC	48
53	Met	Gln	Pro	Asp	Met	Thr	Leu	Asn	Val	Ile	Lys	Met	Lys	Ser	Ser	Asp	
54	1			5					10					15			
55	TTC	CTG	GAG	AGT	ACA	GAA	CTG	GAC	AGC	GGA	GGC	TTT	GGG	AAG	GTG	TCT	96
56	Phe	Leu	Gln	Ser	Ala	Glu	Leu	Asp	Ser	Gly	Gly	Phe	Gly	Lys	Val	Ser	
57				20					25					30			
58	CTG	TGT	TTC	CAC	AGA	AAC	GAG	GGA	CTG	ATG	ATC	ATG	AAA	ACA	GTG	TAC	144
59	Leu	Cys	Phe	His	Arg	Thr	Gln	Gly	Leu	Met	Ile	Met	Lys	Thr	Val	Tyr	
60			35					40					45				
61	AAG	GGG	CCC	AAT	TGC	ATT	GAG	CAC	AAT	GAG	GCT	CTC	TTG	ACG	GAG	GGG	192
62	Lys	Gly	Pro	Asn	Lys	Ile	Gln	His	Asn	Gln	Ala	Leu	Leu	Ile	Gln	Ala	
63		50				55					60						
64	AAG	ATG	ATG	AAC	AGA	CTG	AGA	CAC	AGC	CGG	GTG	GTG	AAG	CTC	CTG	GGC	240
65	Lys	Met	Met	Asn	Arg	Leu	Arg	His	Ser	Arg	Val	Val	Lys	Leu	Leu	Gly	
66		65			70					75			80			85	
67	GTC	ATC	ATA	GAG	GAA	GGG	AAG	TAC	TCC	CTG	GTG	ATG	GAG	TAC	ATG	GAG	288
68	Val	Ile	Ile	Gln	Gln	Gly	Lys	Tyr	Ser	Leu	Val	Met	Gln	Tyr	Met	Gln	
69				85					90				95				
70	AAG	GGC	AAC	CTG	ATG	CAC	GTG	CTG	AAA	GCC	GAG	ATG	AGT	ACT	CCG	CTT	336
71	Lys	Gly	Asn	Leu	Met	His	Val	Leu	Lys	Ala	Gln	Met	Ser	Thr	Pro	Leu	
72			100						105				110				
73	TCT	GTA	AAA	GGA	AGG	ATA	ATT	TTG	GAA	ATC	ATT	GAA	GGA	ATG	TGC	TAC	384
74	Ser	Val	Lys	Gly	Arg	Ile	Ile	Leu	Gln	Ile	Ile	Gln	Gly	Met	Cys	Tyr	
75			115					120					125				
76	TTA	CAT	GGA	AAA	GGC	GTG	ATA	CAC	AAG	GAC	CTG	AAG	CCT	GAA	AAT	ATC	432
77	Leu	His	Gly	Lys	Gly	Val	Ile	His	Lys	Asp	Leu	Lys	Pro	Gln	Asn	Ile	
78		130				135					140						
79	CTT	GTT	GAT	AAT	GAC	TTC	CAC	ATT	AAG	ATC	GCA	GAC	CTC	GGC	CTT	GCC	480
80	Leu	Val	Asp	Asn	Asp	Phe	His	Ile	Lys	Ile	Ala	Asp	Leu	Gly	Leu	Ala	
81	145				150					155				160			
82	TCC	TTT	AAG	ATG	TGG	AGC	AAA	CTG	AAT	AAT	GAA	GAG	CAC	AAT	GAG	CTG	528
83	Ser	Phe	Lys	Met	Trp	Ser	Lys	Leu	Asn	Asn	Gln	Gln	His	Asn	Gln	Leu	
84			165						170				175				
85	AGG	GAA	GTG	GAC	GGC	AAC	GCT	AAG	AAG	AAT	GGC	GGC	ACC	CTC	TAC	TAC	576
86	Arg	Gln	Val	Asp	Gly	Thr	Ala	Lys	Lys	Asn	Gly	Gly	Thr	Leu	Tyr	Tyr	
87			180					185					190				
88	ATG	GCG	CCC	GAG	CAC	CTG	AAT	GAC	GTC	AAC	GCA	AAG	CCC	ACA	GAG	AAG	624
89	Met	Ala	Pro	Gln	His	Leu	Asn	Asp	Val	Asn	Ala	Lys	Pro	Thr	Gln	Lys	
90		195					200					205					
91	TGG	GAT	GTG	TAC	AGC	TTT	GCT	GTA	GTA	CTC	TGG	GCG	ATA	TTT	GCA	AAT	672
92	Ser	Asp	Val	Tyr	Ser	Phe	Ala	Val	Val	Leu	Pro	Ala	Ile	Phe	Ala	Asn	
93		210				215						220					
94	AAG	GAG	CCA	TAT	GAA	AAT	GCT	ATC	TGT	GAG	CAG	CAG	TTG	ATA	ATG	TGC	720
95	Lys	Gln	Pro	Tyr	Gln	Asn	Ala	Ile	Cys	Gln	Gln	Gln	Leu	Ile	Met	Cys	
96		225				230				235			240				
97	ATA	AAA	TCT	GGG	AAC	AGG	CCA	GAT	GTG	GAT	GAC	ATC	ACT	GAG	TAC	TGC	768
98	Ile	Lys	Ser	Gly	Asn	Arg	Pro	Asp	Val	Asp	Asp	Ile	Thr	Gln	Tyr	Cys	
99			245						250				255				
100	CCA	AGA	GAA	ATT	ATC	AGT	CTC	ATG	AAG	CTC	TGC	TGG	GAA	GCG	AAT	CCG	816

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101	Pro	Arg	Glu	Ile	Ile	Ser	Leu	Met	Lys	Leu	Cys	Trp	Glu	Ala	Asn	Pro	
102				260					265					270			
103	GAA	GCT	CGG	CTG	ATA	TTT	TCT	GGT	ATT	GAA	GAA	AAA	TTT	AGG	CCT	TTT	364
104	Glu	Ala	Arg	Pro	Thr	Phe	Pro	Gly	Ile	Glu	Glu	Lys	Ile	Arg	Pro	Phe	
105				275				280					285				
106	TAT	TTA	AGT	CAA	TTA	GAA	GAA	AGT	GTA	GAA	GAG	GAG	CTG	AAG	ACT	TTA	312
107	Tyr	Leu	Ser	Glu	Leu	Glu	Glu	Ser	Val	Glu	Glu	Asp	Val	Lys	Ser	Leu	
108				290				295					300				
109	AAG	AAA	GAG	TAT	TCA	AAC	GAA	AAT	GCA	GTT	CTG	AAG	ACA	ATG	CAG	TTT	360
110	Lys	Lys	Glu	Tyr	Ser	Asn	Glu	Asn	Ala	Val	Val	Lys	Arg	Met	Gln	Ser	
111	305					310						315				320	
112	CTT	CAA	GTT	GAT	TGT	GTG	GCA	GTA	CCT	TCA	AGC	CGG	TCA	AAT	TCA	GTC	1008
113	Leu	Gln	Leu	Asp	Cys	Val	Ala	Val	Pro	Ser	Ser	Arg	Ser	Asn	Ser	Ala	
114					325						330				335		
115	ACA	GAA	CAG	CCT	GST	PCA	CTG	CAC	AGT	TCC	CAG	GGA	CTT	GGG	ATG	GGT	1056
116	Thr	Glu	Gln	Pro	Gly	Ser	Leu	His	Ser	Ser	Gln	Gly	Leu	Gly	Met	Gly	
117					340				345				350				
118	CCT	GTG	GAG	GAG	TCC	TGG	TTT	GCT	CCT	TCC	CTG	GAG	CAC	CCA	CAA	GAA	1104
119	Pro	Val	Glu	Glu	Ser	Trp	Phe	Ala	Pro	Ser	Leu	Glu	His	Pro	Gln	Glu	
120				355				360					365				
121	GAG	AAT	GAG	CCC	ASC	CTG	CAG	AGT	AAA	CTC	CAA	GAC	GAA	GGC	AAC	TAC	1152
122	Glu	Asn	Glu	Pro	Ser	Leu	Gln	Ser	Lys	Leu	Gln	Asp	Glu	Ala	Asn	Tyr	
123				370				375					380				
124	CAT	CTT	TAT	GGC	AGC	CGC	ATG	GAC	AGG	CAG	ACG	AAA	CAG	CAG	CCC	AGA	1200
125	His	Leu	Tyr	Gly	Ser	Arg	Met	Asp	Arg	Gln	Thr	Lys	Gln	Gln	Pro	Arg	
126	385					390						395				400	
127	CAG	AAT	GTG	GCT	TAC	AAC	AGA	GAG	CAG	GAA	AGG	AGA	CGC	AGG	GTC	TCC	1248
128	Gln	Asn	Val	Ala	Tyr	Asn	Arg	Glu	Glu	Glu	Arg	Arg	Arg	Arg	Val	Ser	
129					405						410				415		
130	CAT	GAC	CCT	TTT	GCA	CAG	CAA	AGA	CCT	TAC	GAG	AAT	TTT	CAG	AAT	ACA	1296
131	His	Asp	Pro	Phe	Ala	Gln	Gln	Arg	Pro	Tyr	Glu	Asn	Phe	Gln	Asn	Thr	
132				420					425					430			
133	GAG	GGA	AAA	GGC	ACT	GTT	TAT	TCC	AGT	GCA	GGC	AGT	CAT	GCT	AAT	GCA	1344
134	Glu	Gly	Lys	Gly	Thr	Val	Tyr	Ser	Ser	Ala	Ala	Ser	His	Gly	Asn	Ala	
135				435				440					445				
136	GTG	CAC	CAG	CCC	TCA	GGG	CTC	ACC	AGC	CAA	CCT	CAA	GTA	CTG	TAT	CAG	1392
137	Val	His	Gln	Pro	Ser	Gly	Leu	Thr	Ser	Gln	Pro	Gln	Val	Leu	Tyr	Gln	
138				450				455					460				
139	AAC	AAT	GGA	TTA	TAT	AGC	TCA	CAT	GGC	TTT	GGA	ACA	AGA	CCA	CTG	GAT	1440
140	Asn	Asn	Gly	Leu	Tyr	Ser	Ser	His	Gly	Phe	Gly	Thr	Arg	Pro	Leu	Asp	
141	465					470						475				480	
142	CCA	GGA	ACA	GCA	GST	CCC	AGA	GTT	TGG	TAC	AGG	CCA	ATT	CCA	AGT	CAT	1488
143	Pro	Gly	Thr	Ala	Gly	Pro	Arg	Val	Trp	Tyr	Arg	Pro	Ile	Pro	Ser	His	
144					485						490				495		
145	ATG	CCT	AGT	CTG	CAT	AAT	ATC	CCA	GTG	CCT	GAG	ACC	AAC	TAT	CTA	GGA	1536
146	Met	Pro	Ser	Leu	His	Asn	Ile	Pro	Val	Pro	Glu	Thr	Asn	Tyr	Leu	Gly	
147				500					505					510			
148	AAT	ACA	CCC	ACC	ATG	CCA	TTC	AGC	TCC	TTG	CCA	CCA	ACA	GAT	GAA	TCT	1584
149	Asn	Thr	Pro	Thr	Met	Pro	Phe	Ser	Ser	Leu	Pro	Pro	Thr	Asp	Glu	Ser	

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150          515          520          525
151 ATA AAA TAT ACC ATA TAC AAT AGT AAT GGC ATT CAG ATT GGA GGC TAC      1632
152 Ile Lys Tyr Thr Ile Tyr Asn Ser Thr Gly Ile Gln Ile Gly Ala Tyr
153          530          535          540
154 AAT TAT ATG GAG ATT GGT GGG ACG AST TTA TCA CTA CTA GAT AGC AYA      1680
155 Asn Tyr Met Glu Ile Gly Gly Thr Ser Ser Ser Leu Leu Asp Ser Thr
156 545          550          555          560
157 AAT AAT AAC TTC AAA GAA GAG CCA GGT GGT AAG TAC GAA GGT ATC TTT      1728
158 Asn Thr Asn Phe Lys Gln Gln Pro Ala Ala Lys Tyr Gln Ala Ile Phe
159          565          570          575
160 GAT AAT ACC ACT AGT CTG ACG GAT AAA CAC CTG GAC CCA ATC AGG GAA      1776
161 Asp Asn Thr Thr Ser Leu Phe Asp Lys His Leu Asp Pro Ile Arg Glu
162          580          585          590
163 AAT CTG GGA AAG TAC TGG AAA AAC TGT GGT GGT AAA CTG GGC TTC ACA      1824
164 Asn Leu Gly Lys His Trp Lys Asn Cys Ala Arg Lys Leu Gly Phe Thr
165          595          600          605
166 CAG CCG CAG ATT GAT GAA ATT GAT GAT GAT TAT GAG CGA GAT GGA CTG      1872
167 Gln Ser Gln Ile Asp Gln Ile Asp His Asp Tyr Gln Arg Asp Gly Leu
168          610          615          620
169 AAA GAA AAG GTT TAC CAG ATG CTC CAA AAG TGG GTG ATG AGG GAA GGC      1920
170 Lys Gln Lys Val Tyr Gln Met Leu Gln Lys Trp Val Met Arg Gln Gly
171 6.5          630          635          640
172 ATA AAG GGA GCG ACG CTG GGG AAG CTG GCC CAG GCG CTC CAC CAG TGT      1968
173 Ile Lys Gly Ala Thr Val Gly Lys Leu Ala Gln Ala Leu His Gln Cys
174          645          650          655
175 TCC AGG ATC GAC CTT CTG AGC AGC TTG ATT TAC GTC AGC CAG AAC      2013
176 Ser Arg Ile Asp Leu Leu Ser Ser Leu Ile Tyr Val Ser Gln Asn
177          660          665          670
178 TAA      2016
180 (2) INFORMATION FOR SEQ ID NO: 2:
181 (i) SEQUENCE CHARACTERISTICS:
182 (A) LENGTH: 671 amino acids
183 (B) TYPE: amino acid
184 (C) TOPOLOGY: linear
185 (ii) MOLECULE TYPE: protein
186 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:
187 Met Gln Pro Asp Met Ser Leu Asn Val Ile Lys Met Lys Ser Ser Asp
188 1 5 10 15
189 Phe Leu Gln Ser Ala Gln Leu Asp Ser Gly Gly Phe Gly Lys Val Ser
190 20 25 30
191 Leu Cys Phe His Arg Thr Gln Gly Leu Met Ile Met Lys Thr Val Tyr
192 35 40 45
193 Lys Gly Pro Asn Cys Ile Gln His Asn Glu Ala Leu Leu Glu Glu Ala
194 50 55 60
195 Lys Met Met Asn Arg Leu Arg His Ser Arg Val Val Lys Leu Leu Gly
196 65 70 75 80
197 Val Ile Ile Glu Glu Gly Lys Tyr Ser Leu Val Met Glu Tyr Met Glu
198 85 90 95
199 Lys Gly Asn Leu Met His Val Leu Lys Ala Glu Met Ser Thr Pro Leu

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```

200          100          105          110
201 Ser Val Lys Gly Arg Ile Ile Leu Glu Ile Ile Gln Gly Met Cys Thr
202          115          120          125
203 Leu His Gly Lys Gly Val Ile His Lys Asp Leu Lys Pro Gln Asn Ile
204          130          135          140
205 Leu Val Asp Asn Asp Phe His Leu Lys Ile Ala Asp Leu Gly Leu Ala
206 145          150          155          160
207 Ser Phe Lys Met Trp Ser Lys Leu Asn Asn Glu Glu His Asn Glu Leu
208          165          170          175
209 Arg Glu Val Asp Gly Thr Ala Lys Lys Asn Gly Gly Thr Leu Tyr Tyr
210          180          185          190
211 Met Ala Pro Gln His Leu Asn Asp Val Asn Ala Lys Pro Thr Glu Lys
212          195          200          205
213 Ser Asp Val Tyr Ser Phe Ala Val Val Leu Trp Ala Ile Phe Ala Asn
214          210          215          220
215 Lys Glu Pro Tyr Glu Asn Ala Ile Cys Glu Gln Gln Leu Ile Met Cys
216 225          230          235          240
217 Ile Lys Ser Gly Asn Arg Pro Asp Val Asp Asp Ile Thr Gln Tyr Cys
218          245          250          255
219 Pro Arg Glu Ile Ile Ser Leu Met Lys Leu Cys Trp Glu Ala Asn Pro
220          260          265          270
221 Glu Ala Arg Pro Thr Phe Pro Gly Ile Glu Glu Lys Phe Arg Pro Phe
222          275          280          285
223 Tyr Leu Ser Gln Leu Glu Glu Ser Val Glu Glu Asp Val Lys Ser Leu
224          290          295          300
225 Lys Lys Glu Tyr Ser Asn Glu Asn Ala Val Val Lys Arg Met Gln Ser
226 305          310          315          320
227 Leu Gln Leu Asp Cys Val Ala Val Pro Ser Ser Arg Ser Asn Ser Ala
228          325          330          335
229 Thr Glu Gln Pro Gly Ser Leu His Ser Ser Gln Gly Leu Gly Met Gly
230          340          345          350
231 Pro Val Glu Glu Ser Trp Phe Ala Pro Ser Leu Gln His Pro Gln Gln
232          355          360          365
233 Glu Asn Glu Pro Ser Leu Gln Ser Lys Leu Gln Asp Glu Ala Asn Tyr
234          370          375          380
235 His Leu Tyr Gly Ser Arg Met Asp Arg Gln Thr Lys Gln Gln Pro Arg
236 385          390          395          400
237 Gln Asn Val Ala Tyr Asn Arg Glu Glu Glu Arg Arg Arg Arg Val Ser
238          405          410          415
239 His Asp Pro Phe Ala Gln Gln Arg Pro Tyr Glu Asn Phe Gln Asn Thr
240          420          425          430
241 Glu Gly Lys Gly Thr Val Tyr Ser Ser Ala Ala Ser His Gly Asn Ala
242          435          440          445
243 Val His Gln Pro Ser Gly Leu Thr Ser Gln Pro Gln Val Leu Tyr Gln
244          450          455          460
245 Asn Asn Gly Leu Tyr Ser Ser His Gly Phe Gly Thr Arg Pro Leu Asp
246 465          470          475          480
247 Pro Gly Thr Ala Gly Pro Arg Val Trp Tyr Arg Pro Ile Pro Ser His
248          485          490          495

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VERIFICATION SUMMARY

PATENT APPLICATION: US/09/758,003

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L:24 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]

L:25 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]